

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Covacci, Antonello  
Bugnoli, Massimo  
Telford, John  
Macchia, Giovanni  
Rappuoli, Rino
- (ii) TITLE OF INVENTION: Helicobacter Pylori Proteins Useful  
for Vaccines and Diagnostics
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Chiron Corporation  
(B) STREET: 4560 Horton Street  
(C) CITY: Emeryville  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94608-2916
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/471,491  
(B) FILING DATE: 06-JUNE-1995  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: McClung, Barbara G.  
(B) REGISTRATION NUMBER: 33,113  
(C) REFERENCE/DOCKET NUMBER: 0316.003
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (510) 601-2708  
(B) TELEFAX: (510) 655-3542

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAAGCTTAT CGATGTCGAC TCGAGCT

27

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAAAAGAAAG GAAGAAAATG GAAATACAAC AAACACACCG CAAAATCAAT CGCCCTCTGG	60
TTTCTCTCGC TTTAGTAGGA GCATTAGTCA GCATCACACC GCAACAAAGT CATGCCGCCT	120
TTTTCACAAC CGTGATCATT CCAGCCATTG TTGGGGGTAT CGCTACAGGC ACCGCTGTAG	180
GAACGGTCTC AGGGCTTCTT AGCTGGGGGC TCAAACAAGC CGAAGAAGCC AATAAAACCC	240
CAGATAAACC CGATAAAGTT TGGCGCATT C AAGCAGGAAA AGGCTTTAAT GAATTCCTTA	300
ACAAGGAATA CGACTTATAC AGATCCCTTT TATCCAGTAA GATTGATGGA GGTGCGGATT	360
GGGGGAATGC CGCTAGGCAT TATTGGGTCA AAGGCGGGCA ACAGAATAAG CTTGAAGTGG	420
ATATGAAAGA CGCTGTAGGG ACTTATACCT TATCAGGGCT TAGAACTTT ACTGGTGGGG	480
ATTTAGATGT CAATATGCAA AAAGCCACTT TACGCTTGGG CCAATTCAAT GGCAATTCTT	540
TTACAAGCTA TAAGGATAGT GCTGATCGCA CCACGAGAGT GGATTTCAAC GCTAAAAATA	600
TCTCAATTGA TAATTTTGTA GAAATCAACA ATCGTGTGGG TTCTGGAGCC GGGAGGAAAG	660
CCAGCTCTAC GGTTTTGACT TTGCAAGCTT CAGAAGGGAT CACTAGCGAT AAAAACGCTG	720
AAATTTCTCT TTATGATGGT GCCACGCTCA ATTTGGCTTC AAGCAGCGTT AAATTAATGG	780
GTAATGTGTG GATGGGCCGT TTGCAATACG TGGGAGCGTA TTTGGCCCCT TCATACAGCA	840
CGATAAACAC TTCAAAAGTA ACAGGGGAAG TGAATTTTAA CCACCTCACT GTTGGCGATA	900

AAAACGCCGC TCAAGCGGGC ATTATCGCTA ATAAAAAGAC TAATATTGGC ACACTGGATT	960
TGTGGCAAAG CGCCGGGTTA AACATTATCG CTCCTCCAGA AGGTGGCTAT AAGGATAAAC	1020
CCAATAATAC CCCTTCTCAA AGTGGTGCTA AAAACGACAA AAATGAAAGC GCTAAAAACG	1080
ACAAACAAGA GAGCAGTCAA AATAATAGTA ACACTCAGGT CATTAACCCA CCAATAGTG	1140
CGCAAAAAAC AGAAGTTCAA CCCACGCAAG TCATTGATGG GCCTTTTGCG GGCGGCAAAG	1200
ACACGGTTGT CAATATCAAC CGCATCAACA CTAACGCTGA TGGCACGATT AGAGTGGGAG	1260
GGTTTAAAGC TTCTCTTACC ACCAATGCGG CTCATTTGCA TATCGGCAA GGCGGTGTCA	1320
ATCTGTCCAA TCAAGCGAGC GGGCGCTCTC TTATAGTGGA AAATCTAACT GGAATATCA	1380
CGTTGATGG GCCTTTAAGA GTGAATAATC AAGTGGGTGG CTATGCTTTG GCAGGATCAA	1440
GGCGGAATTT TGAGTTTAAG GCTGGTACGG ATACCAAAAA CGGCACAGCC ACTTTTAATA	1500
ACGATATTAG TCTGGGAAGA TTTGTGAATT TAAAGGTGGA TGCTCATACA GCTAATTTTA	1560
AAGGTATTGA TACGGGTAAT GGTGGTTTCA ACACCTTAGA TTTTAGTGGC GTTACAGACA	1620
AAGTCAATAT CAACAAGCTC ATTACGGCTT CCACTAATGT GGCCGTTAA AACTTCAACA	1680
TTAATGAATT GATTGTAAA ACCAATGGGA TAAGTGTGGG GGAATATACT CATTTTAGCG	1740
AAGATATAGG CAGTCAATCG CGCATCAATA CCGTGC GTTT GGAACTGGC ACTAGGTCAC	1800
TTTCTCTGG GGGTGTTAAA TTAAAGGTG GCGAAAAATT GGTTATAGAT GAGTTTACT	1860
ATAGCCCTTG GAATTATTTT GACGCTAGAA ATATTAAAA TGTTGAAATC ACCAATAAAC	1920
TTGCTTTTGG ACCTCAAGGA AGTCCTTGGG GCACATCAAA ACTTATGTTC AATAATCTAA	1980
CCCTAGGTCA AAATGCGGTC ATGGATTATA GCCAATTTTC AAATTTAACC ATTCAAGGGG	2040
ATTCATCAA CAATCAAGGC ACTATCAACT ATCTGGTCCG AGGTGGGAAA GTGGCAACCT	2100
TAAGCGTAGG CAATGCAGCA GCTATGATGT TTAATAATGA TATAGACAGC GCGACCGGAT	2160
TTTACAAACC GTCATCAAG ATTAACAGCG CTCAAGATCT CATTA AAAAT ACAGAACATG	2220
TTTTATTGAA AGCGAAAATC ATTGGTTATG GTAATGTTTC TACAGGTACC AATGGCATT	2280
GTAATGTAA TCTAGAAGAG CAATTCAAAG AGCGCCTAGC CCTTTATAAC AACATAACC	2340
GCATGGATAC TTGTGTGGTG CGAAATACTG ATGACATTAA AGCATGCGGT ATGGCTATCG	2400
GCGATCAAAG CATGGTGAAC AACCTGACA ATTACAAGTA TCTTATCGGT AAGGCATGGA	2460

AAAATATAGG GATCAGCAAA ACAGCTAATG GCTCTAAAAT TTCGGTGTAT TATTTAGGCA	2520
ATTCTACGCC TACTGAGAAT GGTGGCAATA CCACAAATTT ACCCACAAC ACCACTAGCA	2580
ATGCACGTTT TGCCAACAAC GCCCTTGCAC AAAACGCTCC TTTCGCTCAA CCTAGTGCTA	2640
CTCCTAATTT AGTCGCTATC AATCAGCATG ATTTTGGCAC TATTGAAAGC GTGTTTGAAT	2700
TGGCTAACCG CTCTAAAGAT ATTGACACGC TTTATGCTAA CTCAGGCGCT CAAGGCAGGG	2760
ATCTCTTACA AACCTTATTG ATTGATAGCC ATGATGCGGG TTATGCCAGA AAAATGATTG	2820
ATGCTACAAG CGCTAATGAA ATCACCAAGC AATTGAATAC GGCCACTACC ACTTTAAACA	2880
ACATAGCCAG TTTAGAGCAT AAAACCAGCG GCTTACAAAC TTTGAGCTTG AGTAATGCGA	2940
TCAATTTAAA TTCTCGTTTA GTCAATCTCT CCAGGAGACA CACCAACCAT ATTGACTCGT	3000
TGSCCAAACG CTTACAAGCT TTAAAAGACC AAAAATTCGC TTCTTTAGAA AGCGCGGCAG	3060
AAGTGTGTA TCAATTTGCC CCTAAATATG AAAAACCTAC CAATGTTTGG GCTAACGCTA	3120
TTGGGGGAAC GAGCTTGAAT AATGGCTCTA ACGCTTCATT GTATGGCACA AGCGCGGGCG	3180
TAGACGCTTA CCTTAACGGG CAAGTGGAAG CCATTGTGGG CGGTTTTGGA AGCTATGGTT	3240
ATAGCTCTTT TAATAATCGT GCGAACTCCC TTAAGTCTGG GGCCAATAAC ACTAATTTTG	3300
GCGTGTATAG CCGTATTTTT GCCAACCAGC ATGAATTGGA CTTTGAAGCT CAAGGGGCAC	3360
TAGGGAGCGA TCAATCAAGC TTGAATTTC AAGCGCTCT ATTACAAGAT TTGAATCAAA	3420
GCTATCATTA CTTAGCCTAT AGCGCTGCAA CAAGAGCGAG CTATGGTTAT GACTTCGCGT	3480
TTTTTAGGAA CGCTTTAGTG TTAAAACCAA GCGTGGGTGT GAGCTATAAC CATTTAGGTT	3540
CAACCAACTT TAAAAGCAAC AGCACCAATC AAGTGGCTTT GAAAAATGGC TCTAGCAGTC	3600
AGCATTTATT CAACGCTAGC GCTAATGTGG AAGCGCGCTA TTATTATGGG GACACTTCAT	3660
ACTTCTACAT GAATGCTGGA GTTTTACAAG AGTTCGCTCA TGTTGGCTCT AATAACGCCG	3720
CGTCTTTAAA CACCTTTAAA GTGAATGCCG CTCGCAACCC TTAAATACC CATGCCAGAG	3780
TGATGATGGG TGGGGAATTA AAATTAGCTA AAGAAGTGTT TTTGAATTTG GCGGTTGTTT	3840
ATTTGCACAA TTTGATTTCC AATATAGGCC ATTTGCTTC CAATTTAGGA ATGAGGTATA	3900
GTTTCTAAAT ACCGCTCTTA AACCCTATGCT CAAAGCATGG GTTTGAAATC TTACAAAACA	3960

(2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser  
 1 5 10 15

Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His  
 20 25 30

Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile  
 35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly  
 50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys  
 65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys  
 85 90 95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly  
 100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln  
 115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr  
 130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met  
 145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr  
 165 170 175

Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala  
 180 185 190

Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly  
 195 200 205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala

210		215		220
Ser Glu Gly Ile Thr	225	Ser Asp Lys Asn Ala	230	Glu Ile Ser Leu Tyr Asp
Gly Ala Thr Leu Asn	245	Leu Ala Ser Ser Ser	250	Val Lys Leu Met Gly Asn
Val Trp Met Gly Arg Leu Gln Tyr	260	Val Gly Ala Tyr Leu Ala Pro Ser	265	270
Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn	275	280	285	
His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala	290	295	300	
Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly	305	310	315	320
Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn	325	330	335	
Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala	340	345	350	
Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val	355	360	365	
Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln	370	375	380	
Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile	385	390	395	400
Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe	405	410	415	
Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly	420	425	430	
Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu	435	440	445	
Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn	450	455	460	
Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe	465	470	475	480
Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp	485	490	495	

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala  
 500 505 510  
 Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp  
 515 520 525  
 Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala  
 530 535 540  
 Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val  
 545 550 555 560  
 Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp  
 565 570 575  
 Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr  
 580 585 590  
 Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu  
 595 600 605  
 Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg  
 610 615 620  
 Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln  
 625 630 635 640  
 Gly Ser Pro Trp Gly Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu  
 645 650 655  
 Gly Gln Asn Ala Val Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile  
 660 665 670  
 Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg  
 675 680 685  
 Gly Gly Lys Val Ala Thr Leu Ser Val Gly Asn Ala Ala Ala Met Met  
 690 695 700  
 Phe Asn Asn Asp Ile Asp Ser Ala Thr Gly Phe Tyr Lys Pro Leu Ile  
 705 710 715 720  
 Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys Asn Thr Glu His Val Leu  
 725 730 735  
 Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn Val Ser Thr Gly Thr Asn  
 740 745 750  
 Gly Ile Ser Asn Val Asn Leu Glu Glu Gln Phe Lys Glu Arg Leu Ala  
 755 760 765  
 Leu Tyr Asn Asn Asn Asn Arg Met Asp Thr Cys Val Val Arg Asn Thr

770					775					780					
Asp	Asp	Ile	Lys	Ala	Cys	Gly	Met	Ala	Ile	Gly	Asp	Gln	Ser	Met	Val
785					790					795					800
Asn	Asn	Pro	Asp	Asn	Tyr	Lys	Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn
				805					810					815	
Ile	Gly	Ile	Ser	Lys	Thr	Ala	Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr
			820					825					830		
Leu	Gly	Asn	Ser	Thr	Pro	Thr	Glu	Asn	Gly	Gly	Asn	Thr	Thr	Asn	Leu
		835					840					845			
Pro	Thr	Asn	Thr	Thr	Ser	Asn	Ala	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala
		850					855					860			
Gln	Asn	Ala	Pro	Phe	Ala	Gln	Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala
865					870					875					880
Ile	Asn	Gln	His	Asp	Phe	Gly	Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala
			885						890					895	
Asn	Arg	Ser	Lys	Asp	Ile	Asp	Thr	Leu	Tyr	Ala	Asn	Ser	Gly	Ala	Gln
			900					905					910		
Gly	Arg	Asp	Leu	Leu	Gln	Thr	Leu	Leu	Ile	Asp	Ser	His	Asp	Ala	Gly
		915					920					925			
Tyr	Ala	Arg	Lys	Met	Ile	Asp	Ala	Thr	Ser	Ala	Asn	Glu	Ile	Thr	Lys
		930				935					940				
Gln	Leu	Asn	Thr	Ala	Thr	Thr	Thr	Leu	Asn	Asn	Ile	Ala	Ser	Leu	Glu
945					950					955					960
His	Lys	Thr	Ser	Gly	Leu	Gln	Thr	Leu	Ser	Leu	Ser	Asn	Ala	Met	Ile
				965					970					975	
Leu	Asn	Ser	Arg	Leu	Val	Asn	Leu	Ser	Arg	Arg	His	Thr	Asn	His	Ile
			980					985					990		
Asp	Ser	Phe	Ala	Lys	Arg	Leu	Gln	Ala	Leu	Lys	Asp	Gln	Lys	Phe	Ala
		995					1000					1005			
Ser	Leu	Glu	Ser	Ala	Ala	Glu	Val	Leu	Tyr	Gln	Phe	Ala	Pro	Lys	Tyr
		1010				1015					1020				
Glu	Lys	Pro	Thr	Asn	Val	Trp	Ala	Asn	Ala	Ile	Gly	Gly	Thr	Ser	Leu
1025					1030					1035					1040
Asn	Asn	Gly	Ser	Asn	Ala	Ser	Leu	Tyr	Gly	Thr	Ser	Ala	Gly	Val	Asp
				1045					1050					1055	



Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly Gly Phe Gly Ser  
1060 1065 1070

Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn Ser Leu Asn Ser Gly  
1075 1080 1085

Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn Gln  
1090 1095 1100

His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser  
1105 1110 1115 1120

Ser Leu Asn Phe Lys Ser Ala Leu Leu Gln Asp Leu Asn Gln Ser Tyr  
1125 1130 1135

His Tyr Leu Ala Tyr Ser Ala Ala Thr Arg Ala Ser Tyr Gly Tyr Asp  
1140 1145 1150

Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val  
1155 1160 1165

Ser Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn  
1170 1175 1180

Gln Val Ala Leu Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala  
1185 1190 1195 1200

Ser Ala Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe  
1205 1210 1215

Tyr Met Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn  
1220 1225 1230

Asn Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro  
1235 1240 1245

Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu Ala  
1250 1255 1260

Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile  
1265 1270 1275 1280

Ser Asn Ile Gly His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe  
1285 1290 1295

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCCATTTTA AGCAACTCCA TAGACCACTA AAGAACTTT TTTTGAGGCT ATCTTTGAAA	60
ATCTGTCCTA TTGATTTGTT TTCCATTTTG TTTCCCATGT GGATCTTGTG GATCACAAAC	120
GCTTAATTAT ACATGCTATA GTAAGCATGA CACACAAACC AAAC TATTTT TAGAACGCTT	180
CATGTGCTCA CCTTGACTAA CCATTTCTCC AACCATACTT TAGCGTTGCA TTTGATTTCT	240
TCAAAAAGAT TCATTTCTTA TTTCTTGTTT TTATTAAAGT TCTTTCATTT TAGCAAATTT	300
TTGTTAATTG TGGGTAAAAA TGTGAATCGT CCTAGCCTTT AGACGCCTGC AACGATCGGG	360
GT TTTTTC TAA TATTAATAAT GATTAATGAA AAAAAAAAAA AATGCTTGAT ATTGTTGTAT	420
AATGAGAATG TTCAAAGACA TGAATTGACT ACTCAAGCGT GTAGCGATTT TTAGCAGTCT	480
TTGACACTAA CAAGATACCG ATAGGTATGA AACTAGGTAT AGTAAGGAGA AACAATGACT	540
AACGAAACCA TTGACCAACA ACCACAAACC GAAGCGGCTT TTAACCCGCA GCAATTTATC	600
AATAATCTTC AAGTAGCTTT TCTTAAAGTT GATAACGCTG TCGCTTCATA CGATCCTGAT	660
CAAAAACCAA TCGTTGATAA GAACGATAGG GATAACAGGC AAGCTTTTGA AGGAATCTCG	720
CAATTAAGGG AAGAATACTC CAATAAAGCG ATCAAAAATC CTACCAAAAA GAATCAGTAT	780
TTTTCAGACT TTATCAATAA GAGCAATGAT TTAATCAACA AAGACAATCT CATTGATGTA	840
GAATCTTCCA CAAAGAGCTT TCAGAAATTT GGGGATCAGC GTTACCGAAT TTCACAAGT	900
TGGGTGTCCC ATCAAAACGA TCCGTCTAAA ATCAACACCC GATCGATCCG AAATTTTATG	960
GAAAATATCA TACAACCCCC TATCCTTGAT GATAAAGAGA AAGCGGAGTT TTTGAAATCT	1020
GCCAAACAAT CTTTTGCAGG AATCATTATA GGGAATCAAA TCCGAACGGA TCAAAAGTTC	1080
ATGGGCGTGT TTGATGAGTC CTTGAAAGAA AGGCAAGAAG CAGAAAAAAA TGGAGAGCCT	1140
ACTGGTGGGG ATTGGTTGGA TATTTTTCTC TCATTTATAT TTGACAAAAA ACAATCTTCT	1200
GATGTCAAAG AAGCAATCAA TCAAGAACCA GTTCCCCATG TCCAACCAGA TATAGCCACT	1260
ACCACCACCG ACATACAAGG CTTACCGCCT GAAGCTAGAG ATTTACTTGA TGAAAGGGGT	1320

AATTTTCTA	AATTCACCTCT	TGGCGATATG	GAAATGTAG	ATGTTGAGGG	AGTCGCTGAC	1380
ATTGATCCCA	ATTACAAGTT	CAATCAATTA	TTGATTCACA	ATAACGCTCT	GTCTTCTGTG	1440
TTAATGGGGA	GTCATAATGG	CATAGAACCT	GAAAAAGTTT	CATTGTTGTA	TGGGGGCAAT	1500
GGTGGTCCTG	GAGCTAGGCA	TGATTGGAAC	GCCACCGTTG	GTTATAAAGA	CCAACAAGGC	1560
AACAATGTGG	CTACAATAAT	TAATGTGCAT	ATGAAAAACG	GCAGTGGCTT	AGTCATAGCA	1620
GGTGGTGAGA	AAGGGATTAA	CAACCCTAGT	TTTTATCTCT	ACAAAGAAGA	CCAACTCACA	1680
GGCTCACAAC	GAGCATTAAAG	TCAAGAAGAG	ATCCAAAACA	AAATAGATTT	CATGGAATTT	1740
CTTGACAAA	ATAATGCTAA	ATTAGACAAC	TTGAGCGAGA	AAGAGAAGGA	AAAATTCCGA	1800
ACTGAGATTA	AAGATTTCCA	AAAAGACTCT	AAGGCTTATT	TAGACGCCCT	AGGGAATGAT	1860
CGTATTGCTT	TTGTTTCTAA	AAAAGACACA	AAACATTCAG	CTTTAATTAC	TGAGTTTGGT	1920
AATGGGGATT	TGAGCTACAC	TCTCAAAGAT	TATGGGAAAA	AAGCAGATAA	AGCTTTAGAT	1980
AGGGAGAAAA	ATGTTACTCT	TCAAGGTAGC	CTAAAACATG	ATGGCGTGAT	GTTTGTTGAT	2040
TATTCTAATT	TCAAATACAC	CAACGCCTCC	AAGAATCCCA	ATAAGGGTGT	AGGCGTTACG	2100
AATGGCGTTT	CCCATTTAGA	AGTAGGCTTT	AACAAGGTAG	CTATCTTTAA	TTTGCCTGAT	2160
TTAAATAATC	TCGCTATCAC	TAGTTTCGTA	AGGCGGAATT	TAGAGGATAA	ACTAACCACT	2220
AAAGGATTGT	CCCCACAAGA	AGCTAATAAG	CTTATCAAAG	ATTTTTTGAG	CAGCAACAAA	2280
GAATTGGTTG	GAAAAACTTT	AAACTTCAAT	AAAGCTGTAG	CTGACGCTAA	AAACACAGGC	2340
AATTATGATG	AAGTGAAAAA	AGCTCAGAAA	GATCTTGAAA	AATCTCTAAG	GAAACGAGAG	2400
CATTTAGAGA	AAGAAGTAGA	GAAAAAATTG	GAGAGCAAAA	GCGGCAACAA	AAATAAAATG	2460
GAAGCAAAAG	CTCAAGCTAA	CAGCCAAAAA	GATGAGATTT	TTGCGTTGAT	CAATAAAGAG	2520
GCTAATAGAG	ACGCAAGAGC	AATCGCTTAC	GCTCAGAATC	TTAAAGGCAT	CAAAGGGGAA	2580
TTGTCTGATA	AACTTGAAAA	TGTCAACAAG	AATTTGAAAG	ACTTTGATAA	ATCTTTTGAT	2640
GAATTCAAAA	ATGGCAAAAA	TAAGGATTTT	AGCAAGGCAG	AAGAAACACT	AAAAGCCCTT	2700
AAAGGTTTCG	TGAAAGATTT	AGGTATCAAT	CCAGAATGGA	TTTCAAAAGT	TGAAAACCTT	2760
AATGCAGCTT	TGAATGAATT	CAAAAATGGC	AAAAATAAGG	ATTTCAGCAA	GGTAACGCAA	2820
GCAAAAAGCG	ACCTTGAAAA	TTCCGTTAAA	GATGTGATCA	TCAATCAAAA	GGTAACGGAT	2880

AAAGTTGATA ATCTCAATCA AGCGGTATCA GTGGCTAAAG CAACGGGTGA TTTCAGTAGG	2940
GTAGAGCAAG CGTTAGCCGA TCTCAAAAAT TTCTCAAAGG AGCAATTGGC CCAACAAGCT	3000
CAAAAAAATG AAAGTCTCAA TGCTAGAAAA AAATCTGAAA TATATCAATC CGTTAAGAAT	3060
GGTGTGAATG GAACCCTAGT CGGTAATGGG TTATCTCAAG CAGAAGCCAC AACTCTTTCT	3120
AAAAACTTTT CGGACATCAA GAAAGAGTTG AATGCAAAAC TTGGAAATTT CAATAACAAT	3180
AACAATAATG GACTCAAAAA CGAACCCATT TATGCTAAAG TTAATAAAAA GAAAGCAGGG	3240
CAAGCAGCTA GCCTTGAAGA ACCCATTTAC GCTCAAGTTG CTAAAAAGGT AAATGCAAAA	3300
ATTGACCGAC TCAATCAAAT AGCAAGTGGT TTGGGTGTTG TAGGGCAAGC AGCGGGCTTC	3360
CCTTTGAAAA GGCATGATAA AGTTGATGAT CTCAGTAAGG TAGGGCTTTC AAGGAATCAA	3420
GAATTGGCTC AGAAAATTGA CAATCTCAAT CAAGCGGTAT CAGAAGCTAA AGCAGGTTTT	3480
TTTGGCAATC TAGAGCAAAC GATAGACAAG CTCAAAGATT CTACAAAACA CAATCCCATG	3540
AATCTATGGG TTGAAAGTGC AAAAAAAGTA CCTGCTAGTT TGTCAGCGAA ACTAGACAAT	3600
TACGCTACTA ACAGCCACAT ACGCATTAAT AGCAATATCA AAAATGGAGC AATCAATGAA	3660
AAAGCGACCG GCATGCTAAC GCAAAAAAAC CCTGAGTGGC TCAAGCTCGT GAATGATAAG	3720
ATAGTTGCGC ATAATGTAGG AAGCGTTCCT TTGTCAGAGT ATGATAAAAT TGGCTTCAAC	3780
CAGAAGAATA TGAAAGATTA TTCTGATTCG TTCAAGTTTT CCACCAAGTT GAACAATGCT	3840
GTAAAAGACA CTAATTCTGG CTTTACGCAA TTTTTAACCA ATGCATTTTC TACAGCATCT	3900
TATTACTGCT TGGCGAGAGA AAATGCGGAG CATGGAATCA AGAACGTAA TACAAAAGGT	3960
GGTTTCCAA AATCTTAAAG GATTAAGGAA TACCAAAAAC GCAAAAACCA CCCCTTGCTA	4020
AAAGCGAGGG GTTTTTTAAT ACTCCTTAGC AGAAATCCCA ATCGTCTTTA GTATTTGGGA	4080
TGAATGCTAC CAATTCATGG TATCATATCC CCATACATTC GTATCTAGCG TAGGAAGTGT	4140
GCAAAGTTAC GCCTTTGGAG ATATGATGTG TGAGACCTGT AGGGAATGCG TTGGAGCTCA	4200
AACTCTGTAA AATCCCTATT ATAGGGACAC AGAGTGAGAA CCAAACCTCTC CCTACGGGCA	4260
ACATCAGCCT AGGAAGCCCA ATCGTCTTTA GCGGTTGGGC ACTTCACCTT AAAATATCCC	4320
GACAGACACT AACGAAAGGC TTTGTTCTTT AAAGTCTGCA TGGATATTTT CTACCCCAA	4380
AAGACTTAAC CCTTTGCTTA AAATTAAGTT TGATTGTGCT AGTGGGTTCG TGCTATAGTG	4440

CGAAAATTAA	TTAAGGGTTA	TAAAGAGAGC	ATAAACTAGA	AAAAACAAGT	AGCTATAACA	4500
AAGATCAAGT	TCAAAAAATC	ATAGAGCTTT	TAGAGCAAAT	TGATCGCGCT	CTTAACCAAA	4560
GAAAAATCAG	AAAAACCATA	GGAATTATCA	CACCTTATAA	TGCCCAAAAA	AGACGCTTGC	4620
GATCAGAAGT	GGAAAAATAC	GGCTTCAAGA	ATTTTGATGA	GCTCAAAATA	GACACTGTGG	4680
ATGCCTTTCA	AGGTGAAGAG	GCAGATATTA	TTATTTATTC	CACCGTGAAA	ACTTGTGGTA	4740
ATCTTTCTTT	CTTGCTAGAT	TCTAAACGCT	TGAATGTGGC	TATTTCTAGG	GCAAAAGAAA	4800
ATCTCATTTT	TGTGGGTAAA	AAGTCTTTCT	TTGAGAATTT	ATGAAGCGAT	GAGAAGAATA	4860
TCTTTAGCGC	TATTTTGCAA	GTCTGTAGAT	AGGTAATCTT	TTCCAAAGAT	AATCATTAGA	4920
CATTCTTCGC	TTCAAAACGC	TTTCATAAAT	CTCTCTAAAG	CGCTTTATAA	TCAACACAAT	4980
AGCCTTATAG	TGTGAGCTAT	AGCCCCTTTT	TGGGAATTGA	GTTATTTTGA	CTTTAAATTT	5040
TTATTAGCGT	TACAATTTGA	GCCATTCTTT	AGCTTGTTTT	TCTAGCCAGA	TCACATCGCC	5100
GCTCGCATGA	AATTCCACTT	TAGGGAATGC	GTGTGCATTT	TTTTTAAGGG	CGTATTTTTG	5160
CTGCAAATAT	CCTACAATAG	CATCGCCCGA	ATGGATGAGT	AGGGGGGGTG	TTGAAAGGGC	5220
AAAATGCTCC	ATAAAATAGC	CCTCAATTTT	TTGAGCGATT	AAGGGAAAAT	GCGTGCAACC	5280
TAAATAATC	ACTTCGGGAA	AATCTTTAAG	GGAGTGAAAT	AATAACGCAT	GCAAGTTTCT	5340
AACAATTCGC	CCTCTAAAT	ACTTTCTTCA	ATCAAAGGCA	CAAAAAGAGA	AGTGGCTAAA	5400
TGCGAAACAT	TCAAATAGCC	TTGTTGTTTC	AGGGCATTGT	CATAAGCGTT	GGATTGGATC	5460
GTCGCTTTTG	TCCCTAGCAC	TAAAATAGGG	GCGTTTTTAT	CTTTTACTTG	TCGCTTGATC	5520
GCTAAAATGC	TTGGCTCAAT	CACGCCCACA	ATAGGGATTT	TGGAATGCTT	TTGCATCTCT	5580
TCTAAAGCTA	GAGCGCTCGC	TGTGTTGCAT	GCCACAATCA	ATAATTCAAT	CTGGTGCGGT	5640
TTGAAAAAAT	CCAAAGCCTC	TAAGCCAAAT	TGCTTGATCG	TAGTGGGGTC	TTTAGTGCCA	5700
TAAGGCACTC	TAGCCGTATC	GCCATAATAG	ATGATTTTCAT	CAAATAATTG	CGCTTTTAAA	5760
AGGCTTTTTA	AAACGCTAAA	CCCTCCCACA	CCGCTATCAA	AAACGCCTAT	TTTCATGACA	5820
CTTTTTTAAT	TTAATGGGAT	TAATTAGGGA	TTTTATTTTT	CATTCATTAA	GTTTAAAAAT	5880
TCTTCATTGT	CCTTAGTTTG	TTGCATTTTA	GAATAGACAA	AGCTT		5925

(2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Thr Asn Glu Thr Ile Asp Gln Gln Pro Gln Thr Glu Ala Ala Phe  
1 5 10 15  
Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Leu Lys Val  
20 25 30  
Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp  
35 40 45  
Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Gly Ile Ser Gln Leu  
50 55 60  
Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn  
65 70 75 80  
Gln Tyr Phe Ser Asp Phe Ile Asn Lys Ser Asn Asp Leu Ile Asn Lys  
85 90 95  
Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys Ser Phe Gln Lys Phe  
100 105 110  
Gly Asp Gln Arg Tyr Arg Ile Phe Thr Ser Trp Val Ser His Gln Asn  
115 120 125  
Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg Asn Phe Met Glu Asn  
130 135 140  
Ile Ile Gln Pro Pro Ile Leu Asp Asp Lys Glu Lys Ala Glu Phe Leu  
145 150 155 160  
Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile  
165 170 175  
Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu  
180 185 190  
Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Thr Gly Gly Asp Trp Leu  
195 200 205  
Asp Ile Phe Leu Ser Phe Ile Phe Asp Lys Lys Gln Ser Ser Asp Val

210					215					220					
Lys	Glu	Ala	Ile	Asn	Gln	Glu	Pro	Val	Pro	His	Val	Gln	Pro	Asp	Ile
225					230					235					240
Ala	Thr	Thr	Thr	Thr	Asp	Ile	Gln	Gly	Leu	Pro	Pro	Glu	Ala	Arg	Asp
				245					250					255	
Leu	Leu	Asp	Glu	Arg	Gly	Asn	Phe	Ser	Lys	Phe	Thr	Leu	Gly	Asp	Met
			260					265					270		
Glu	Met	Leu	Asp	Val	Glu	Gly	Val	Ala	Asp	Ile	Asp	Pro	Asn	Tyr	Lys
		275					280					285			
Phe	Asn	Gln	Leu	Leu	Ile	His	Asn	Asn	Ala	Leu	Ser	Ser	Val	Leu	Met
	290					295					300				
Gly	Ser	His	Asn	Gly	Ile	Glu	Pro	Glu	Lys	Val	Ser	Leu	Leu	Tyr	Gly
305					310					315					320
Gly	Asn	Gly	Gly	Pro	Gly	Ala	Arg	His	Asp	Trp	Asn	Ala	Thr	Val	Gly
				325					330					335	
Tyr	Lys	Asp	Gln	Gln	Gly	Asn	Asn	Val	Ala	Thr	Ile	Ile	Asn	Val	His
			340					345					350		
Met	Lys	Asn	Gly	Ser	Gly	Leu	Val	Ile	Ala	Gly	Gly	Glu	Lys	Gly	Ile
		355				360						365			
Asn	Asn	Pro	Ser	Phe	Tyr	Leu	Tyr	Lys	Glu	Asp	Gln	Leu	Thr	Gly	Ser
		370				375					380				
Gln	Arg	Ala	Leu	Ser	Gln	Glu	Glu	Ile	Gln	Asn	Lys	Ile	Asp	Phe	Met
385					390					395					400
Glu	Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Glu	Lys
				405					410					415	
Glu	Lys	Glu	Lys	Phe	Arg	Thr	Glu	Ile	Lys	Asp	Phe	Gln	Lys	Asp	Ser
			420					425					430		
Lys	Ala	Tyr	Leu	Asp	Ala	Leu	Gly	Asn	Asp	Arg	Ile	Ala	Phe	Val	Ser
		435					440					445			
Lys	Lys	Asp	Thr	Lys	His	Ser	Ala	Leu	Ile	Thr	Glu	Phe	Gly	Asn	Gly
	450					455					460				
Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala
465					470					475					480
Leu	Asp	Arg	Glu	Lys	Asn	Val	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp
				485					490					495	

Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser  
 500 505 510  
 Lys Asn Pro Asn Lys Gly Val Gly Val Thr Asn Gly Val Ser His Leu  
 515 520 525  
 Glu Val Gly Phe Asn Lys Val Ala Ile Phe Asn Leu Pro Asp Leu Asn  
 530 535 540  
 Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn Leu Glu Asp Lys Leu  
 545 550 555 560  
 Thr Thr Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Ile Lys Asp  
 565 570 575  
 Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Thr Leu Asn Phe Asn  
 580 585 590  
 Lys Ala Val Ala Asp Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys  
 595 600 605  
 Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg Lys Arg Glu His Leu  
 610 615 620  
 Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys Ser Gly Asn Lys Asn  
 625 630 635 640  
 Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe  
 645 650 655  
 Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr  
 660 665 670  
 Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu  
 675 680 685  
 Asn Val Asn Lys Asn Leu Lys Asp Phe Asp Lys Ser Phe Asp Glu Phe  
 690 695 700  
 Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys  
 705 710 715 720  
 Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile  
 725 730 735  
 Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly  
 740 745 750  
 Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu  
 755 760 765  
 Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr Asp Lys Val



770					775					780					
Asp 785	Asn	Leu	Asn	Gln	Ala 790	Val	Ser	Val	Ala	Lys 795	Ala	Thr	Gly	Asp	Phe 800
Ser	Arg	Val	Glu	Gln 805	Ala	Leu	Ala	Asp	Leu 810	Lys	Asn	Phe	Ser	Lys 815	Glu
Gln	Leu	Ala	Gln 820	Gln	Ala	Gln	Lys	Asn 825	Glu	Ser	Leu	Asn	Ala	Arg	Lys
Lys	Ser	Glu 835	Ile	Tyr	Gln	Ser	Val 840	Lys	Asn	Gly	Val	Asn 845	Gly	Thr	Leu
Val	Gly 850	Asn	Gly	Leu	Ser	Gln 855	Ala	Glu	Ala	Thr	Thr 860	Leu	Ser	Lys	Asn
Phe 865	Ser	Asp	Ile	Lys	Lys 870	Glu	Leu	Asn	Ala	Lys 875	Leu	Gly	Asn	Phe	Asn 880
Asn	Asn	Asn	Asn	Asn 885	Gly	Leu	Lys	Asn	Glu 890	Pro	Ile	Tyr	Ala	Lys 895	Val
Asn	Lys	Lys	Lys 900	Ala	Gly	Gln	Ala	Ala 905	Ser	Leu	Glu	Glu 910	Pro	Ile	Tyr
Ala	Gln 915	Val	Ala	Lys	Lys	Val	Asn 920	Ala	Lys	Ile	Asp	Arg 925	Leu	Asn	Gln
Ile 930	Ala	Ser	Gly	Leu	Gly	Val 935	Val	Gly	Gln	Ala	Ala 940	Gly	Phe	Pro	Leu
Lys 945	Arg	His	Asp	Lys	Val 950	Asp	Asp	Leu	Ser	Lys 955	Val	Gly	Leu	Ser	Arg 960
Asn	Gln	Glu	Leu	Ala 965	Gln	Lys	Ile	Asp	Asn 970	Leu	Asn	Gln	Ala	Val 975	Ser
Glu	Ala	Lys	Ala 980	Gly	Phe	Phe	Gly	Asn 985	Leu	Glu	Gln	Thr	Ile 990	Asp	Lys
Leu	Lys	Asp 995	Ser	Thr	Lys	His	Asn 1000	Pro	Met	Asn	Leu	Trp 1005	Val	Glu	Ser
Ala 1010	Lys	Lys	Val	Pro	Ala	Ser	Leu 1015	Ser	Ala	Lys	Leu	Asp 1020	Asn	Tyr	Ala
Thr 1025	Asn	Ser	His	Ile	Arg 1030	Ile	Asn	Ser	Asn 1035	Ile	Lys	Asn	Gly	Ala	Ile 1040
Asn	Glu	Lys	Ala	Thr 1045	Gly	Met	Leu	Thr	Gln 1050	Lys	Asn	Pro	Glu	Trp 1055	Leu

Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Pro  
 1060 1065 1070

Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp  
 1075 1080 1085

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val Lys  
 1090 1095 1100

Asp Thr Asn Ser Gly Phe Thr Gln Phe Leu Thr Asn Ala Phe Ser Thr  
 1105 1110 1115 1120

Ala Ser Tyr Tyr Cys Leu Ala Arg Glu Asn Ala Glu His Gly Ile Lys  
 1125 1130 1135

Asn Val Asn Thr Lys Gly Gly Phe Gln Lys Ser  
 1140 1145

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe  
 1 5 10 15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro  
 20 25 30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile  
 35 40 45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro  
 50 55 60

Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr  
 65 70 75 80

Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr  
 85 90 95

Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro  
 100 105 110

Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn  
 115 120 125  
 Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr  
 130 135 140  
 Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu  
 145 150 155 160  
 Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val  
 165 170 175  
 Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met  
 180 185 190  
 Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu  
 195 200 205  
 Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys  
 210 215 220  
 Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met  
 225 230 235 240  
 Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu  
 245 250 255  
 Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile  
 260 265 270  
 Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu  
 275 280 285  
 Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu  
 290 295 300  
 Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly  
 305 310 315 320  
 Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly  
 325 330 335  
 His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile  
 340 345 350  
 Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu  
 355 360 365  
 Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser  
 370 375 380  
 Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser

385		390		395		400
Ala Thr Lys	Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala	405	410	415		
Ala Leu Ile Arg	Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp	420	425	430		
Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu		435	440	445		
Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn		450	455	460		
Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly		465	470	475	480	
Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val		485	490	495		
Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu		500	505	510		
Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro		515	520	525		
Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly		530	535	540		
Met Met		545				

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTTGCTG TCATGATCAC AAAAAACACT AAAAAACATT ATTATTAAGG ATACAAAATG	60
GCAAAAGAAA TCAAATTTTC AGATAGTGCG AGAAACCTTT TATTTGAAGG CGTGAGGCAA	120
CTCCATGACG CTGTCAAAGT AACCATGGGG CCAAGAGGCA GGAATGTATT GATCCAAAAA	180

AGCTATGGCG	CTCCAAGCAT	CACCAAAGAC	GGCGTGAGCG	TGGCTAAAGA	GATTGAATTA	240
AGTTGCCCAG	TAGCTAACAT	GGGCGCTCAA	CTCGTTAAAG	AAGTAGCGAG	CAAAACCGCT	300
GATGCTGCCG	GCGATGGCAC	GACCACAGCG	ACCGTGCTAG	CTTATAGCAT	TTTTAAAGAA	360
GGTTTGAGGA	ATATCACGGC	TGGGGCTAAC	CCTATTGAAG	TGAAACGAGG	CATGGATAAA	420
GCTGCTGAAG	CGATCATTA	TGAGCTTAAA	AAAGCGAGCA	AAAAAGTAGG	CGGTAAAGAA	480
GAAATCACCC	AAGTGCGGAC	CATTTCTGCA	AACTCCGATC	ACAATATCGG	GAAACTCATC	540
GCTGACGCTA	TGGAAAAAGT	GGGTAAAGAC	GGCGTGATCA	CCGTTGAGGA	AGCTAAGGGC	600
ATTGAAGATG	AATTGGATGT	CGTAGAAGGC	ATGCAATTTG	ATAGAGGCTA	CCTCTCCCCT	660
TATTTTGTAA	CGAACGCTGA	GAAAATGACC	GCTCAATTGG	ATAATGCTTA	CATCCTTTTA	720
ACGGATAAAA	AAATCTCTAG	CATGAAAGAC	ATTCTCCCGC	TACTAGAAAA	AACCATGAAA	780
GAGGGCAAAC	CGCTTTTAAT	CATCGCTGAA	GACATTGAGG	GCGAAGCTTT	AACGACTCTA	840
GTGGTGAATA	AATTAAGAGG	CGTGTTGAAT	ATCGCAGCGG	TTAAAGCTCC	AGGCTTTGGG	900
GACAGAAGAA	AAGAAATGCT	CAAAGACATC	GCTATTTTAA	CCGGCGGTCA	AGTCATTAGC	960
GAAGAATTGG	GCTTGAGTCT	AGAAAACGCT	GAAGTGGAGT	TTTtagGCAA	AGCTGGAAGG	1020
ATTGTGATTG	ACAAAGACAA	CACCACGATC	GTAGATGGCA	AAGGCCATAG	CGATGATGTT	1080
AAAGACAGAG	TCGCGCAGAT	CAAAACCCAA	ATTGCAAGTA	CGACAAGCGA	TTATGACAAA	1140
GAAAAATTGC	AAGAAAGATT	GGCTAAACTC	TCTGGCGGTG	TGGCTGTGAT	TAAAGTGGGC	1200
GCTGCGAGTG	AAGTGGAAT	GAAAGAGAAA	AAAGACCGGG	TGGATGACGC	GTTGAGCGCG	1260
ACTAAAGCGG	CGGTTGAAGA	AGGCATTGTG	ATTGGTGGCG	GTGCGGCTCT	CATTCGCGCG	1320
GCTCAAAAAG	TGCATTTGAA	TTTGCACGAT	GATGAAAAAG	TGGGCTATGA	AATCATCATG	1380
CGCGCCATTA	AAGCCCCATT	AGCTCAAATC	GCTATCAACG	CTGGTTATGA	TGGCGGTGTG	1440
GTCGTGAATG	AAGTAGAAAA	ACACGAAGGG	CATTTTGTTT	TTAACGCTAG	CAATGGCAAG	1500
TATGTGGATA	TGTTTAAAGA	AGGCATTATT	GACCCCTTAA	AAGTAGAAAG	GATCGCTCTA	1560
CAAAATGCGG	TTTCGGTTTC	AAGCCTGCTT	TTAACCACAG	AAGCCACCGT	GCATGAAATC	1620
AAAGAAGAAA	AAGCGACTCC	GGCAATGCCT	GATATGGGTG	GCATGGGCGG	TATGGGAGGC	1680
ATGGGCGGCA	TGATGTAAGC	CCGCTTGCTT	TTTAGTATAA	TCTGCTTTTA	AAATCCCTTC	1740

TCTAAATCCC CCCCTTTCTA AAATCTCTTT TTTGGGGGGG TGCTTTGATA AAACCGCTCG 1800

CTTGTA AAAA CATGCAACAA AAAATCTCTG TTAAGCTT 1838